

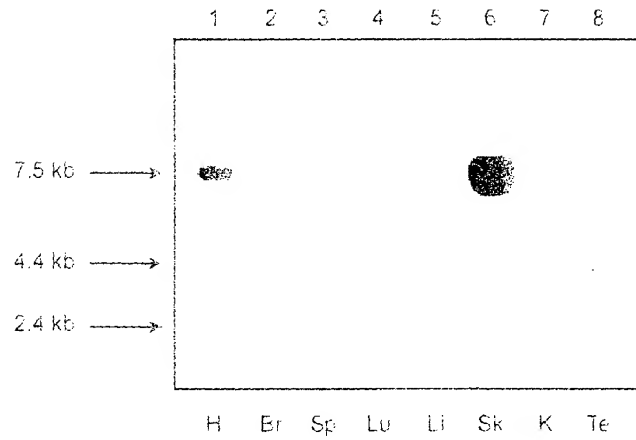
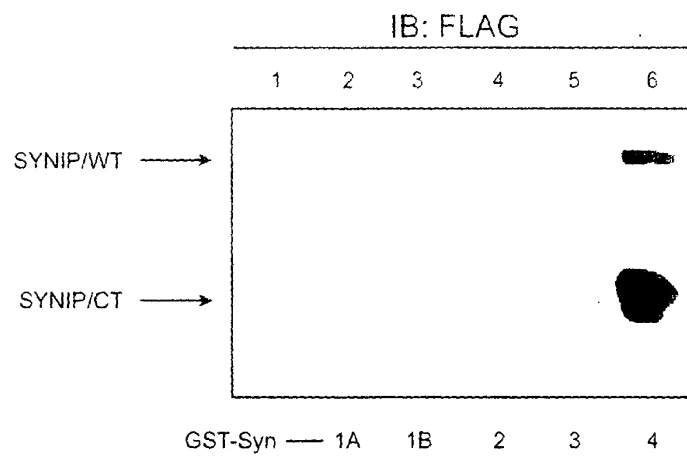
FIG-1A SYNIP AMINO ACID SEQUENCE

1	MSDGTASARS	SSPLDRDPAF	RVITVTKETG	LGLKILGGIN	RNEGPLVYIH	EVIPGGDCYK	DGRKPGDQL	70
71	VSINKESMIG	VSFEFAKSII	TRAKLRSESP	WEIAFIROKS	YCGHPGNICC	PSPQVSEDCG	POTSTFTLLS	140
141	SPSETLLPKT	SSTPQTQDST	FPSCKAIQTK	PEHDKTEHSP	ITSLDNSPAD	TSNADIAPAW	TDDDSGPQ GK	210
211	ISLNPSVRLK	AEKLEMAINY	LGIQPTKEQR	EALREQVQAD	SKGTVSFGDF	VQVARSIFCL	QLDEVNVGVH	280
281	EIPSILDSQL	LPCDLSLEADE	VGKLRQERNA	ALEERNVLKE	KLLESEKHRK	QLIEELQNVK	QEA KAVAEET	350
351	RALRSRIHLA	EAAQROAHGM	EMDYEEVIRL	LEAEVSELKA	QLADYSDONK	ESVQDLRKRV	TVLDCQLRKS	420
421	EMARKAFKAS	TERLLGFIEA	IQEVLLDSSA	PLSTLSERRA	VLASQTSIPL	LARNGRSFPA	TLLESKELV	490
491	RSVRAILDMD	CLPYGWEEAY	TADGIKYFIN	HVTQTTSWIH	PVMSALNLSC	AESEEDCPR	ELTDPKS	557

FIG-1B SYNIP DOMAIN STRUCTURE

19	93	219	264	300	410	500	533
	PDZ		EF		CC	CC	WW

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FIG-1C NORTHERN BLOTFIG-1D BINDING SPECIFICITY

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FIG-2A LYSATE

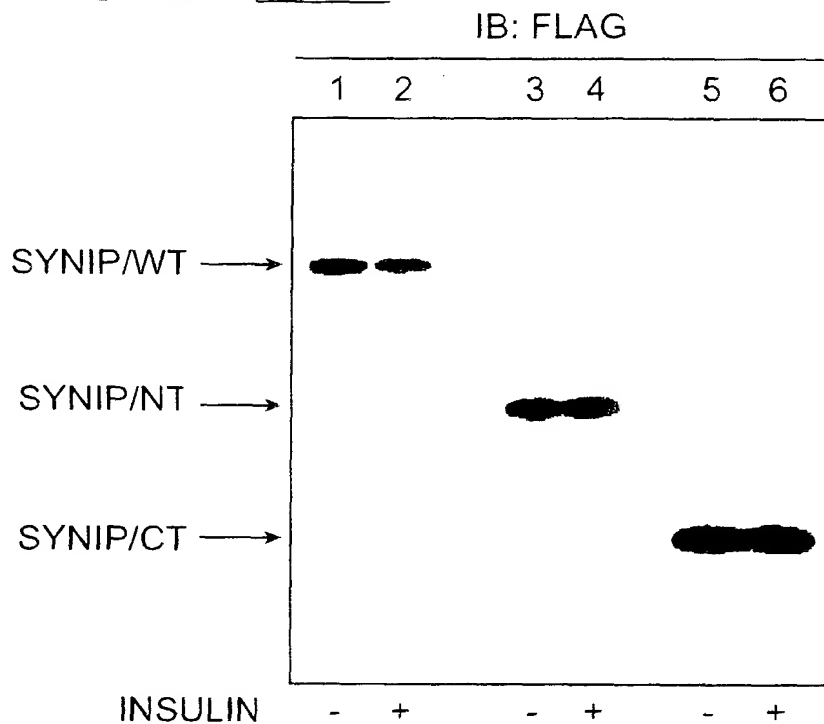
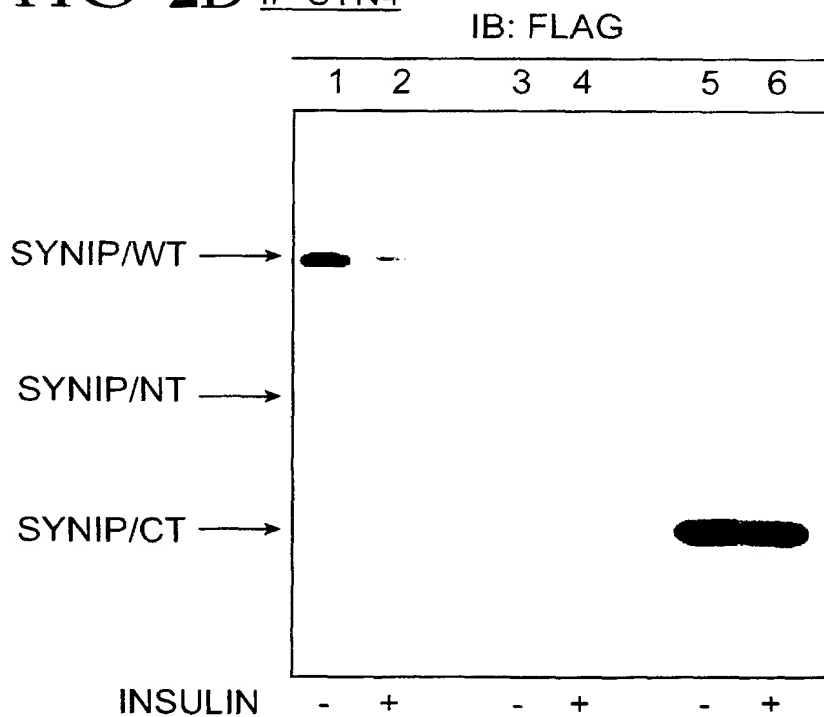
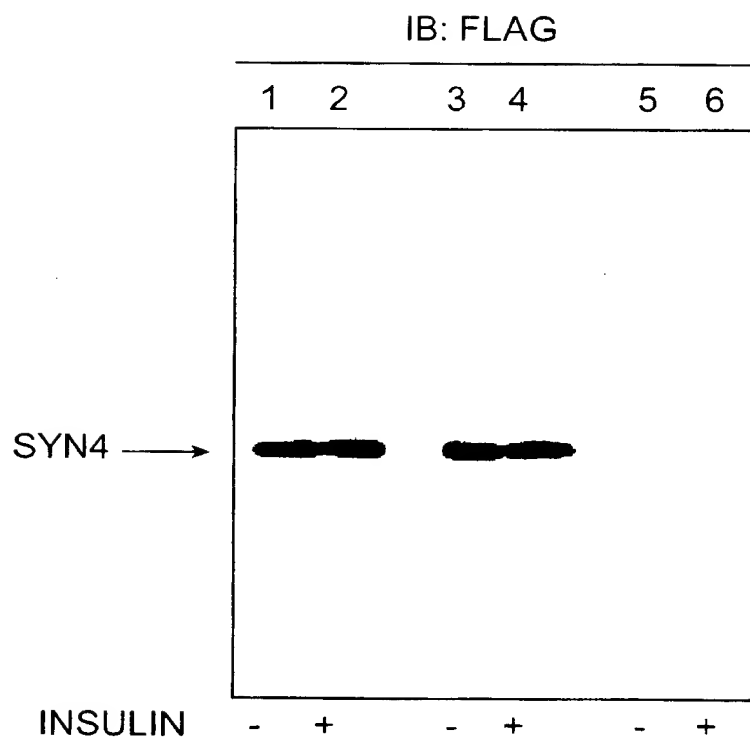


FIG-2B IP-SYN4



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FIG-2C IP-SYN4

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FIG-3A LYSATE

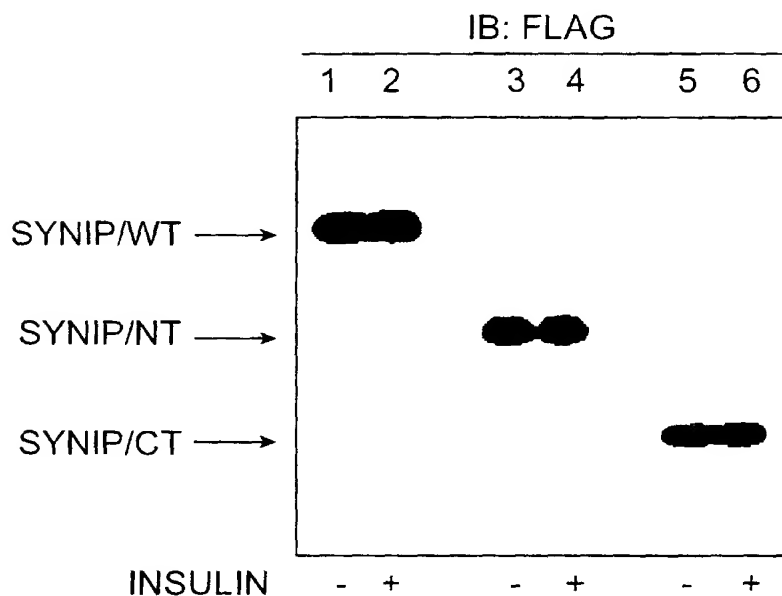
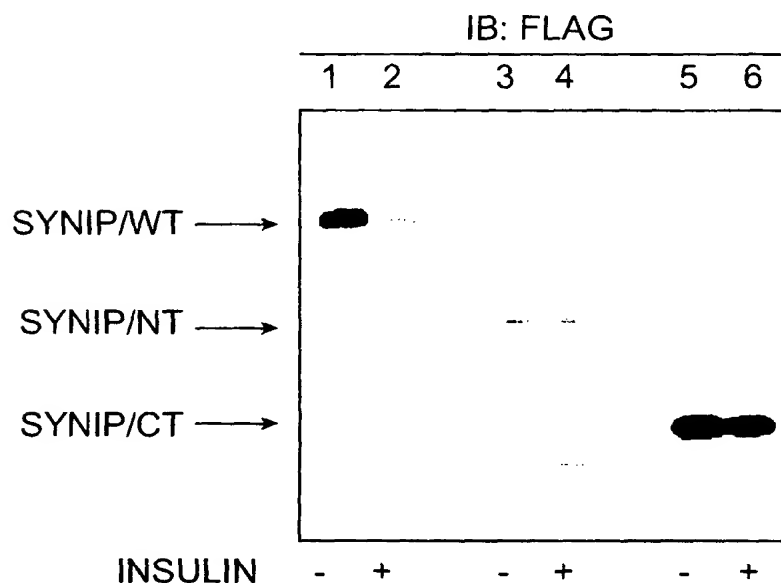
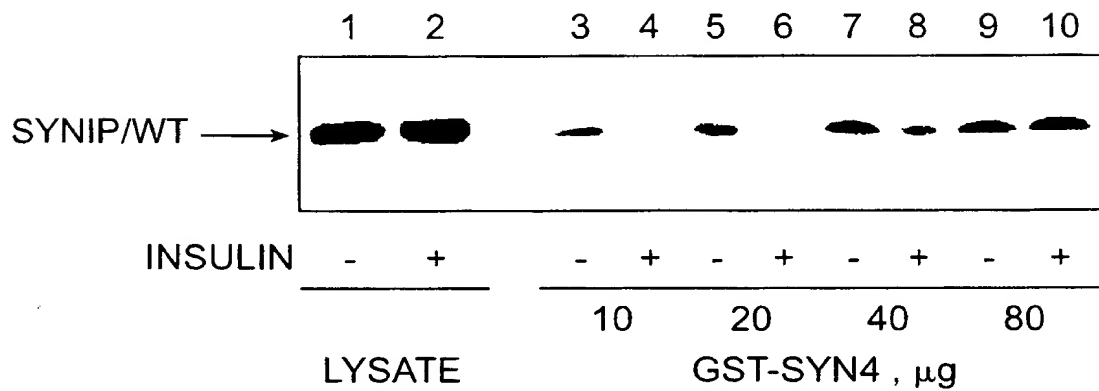


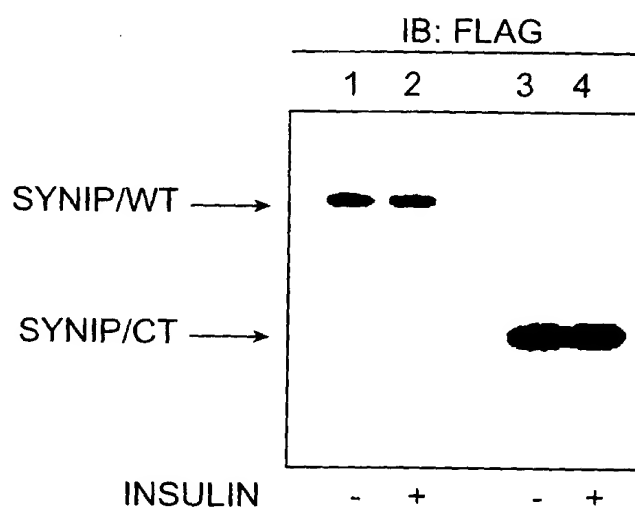
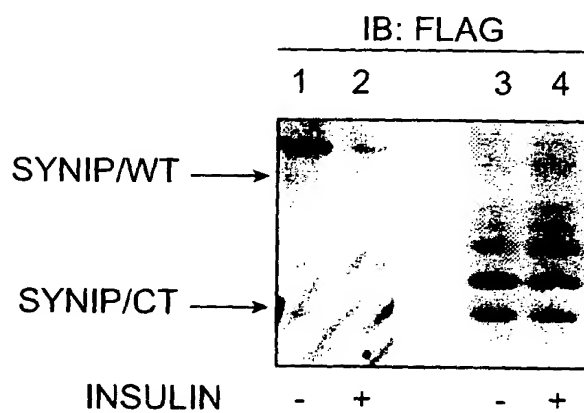
FIG-3B GST-SYN4



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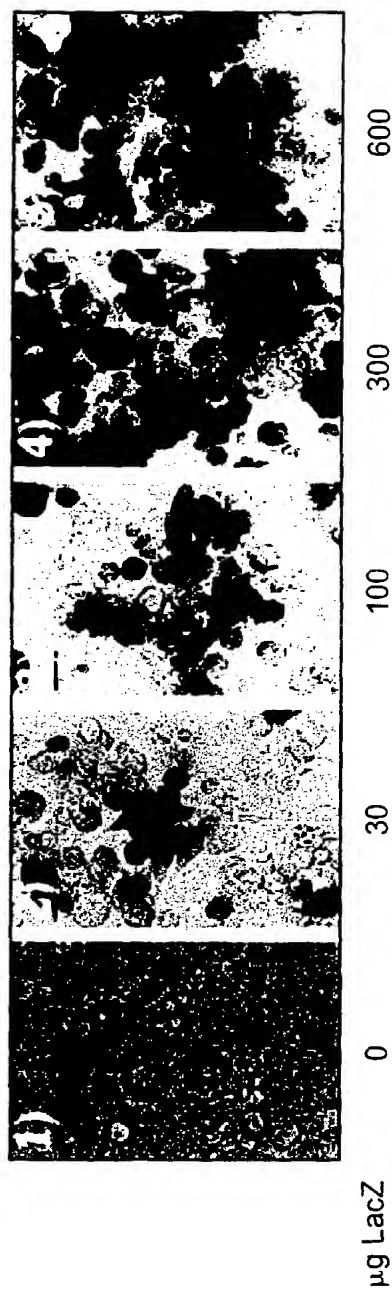
FIG-3C GST-SYNIPFIG-3D IB: FLAG

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FIG-4A LYSATEFIG-4B GST-SYN4

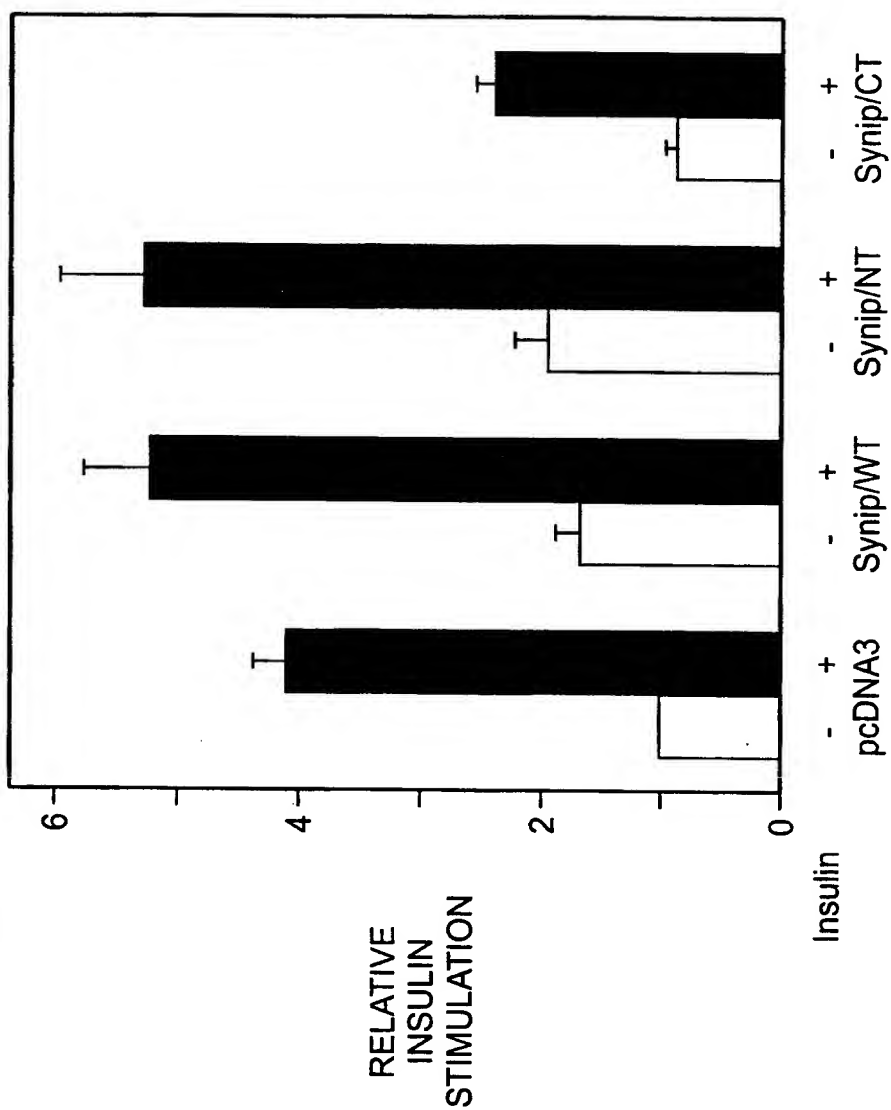
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FIG-5A β -GALACTOSIDASE EXPRESSION



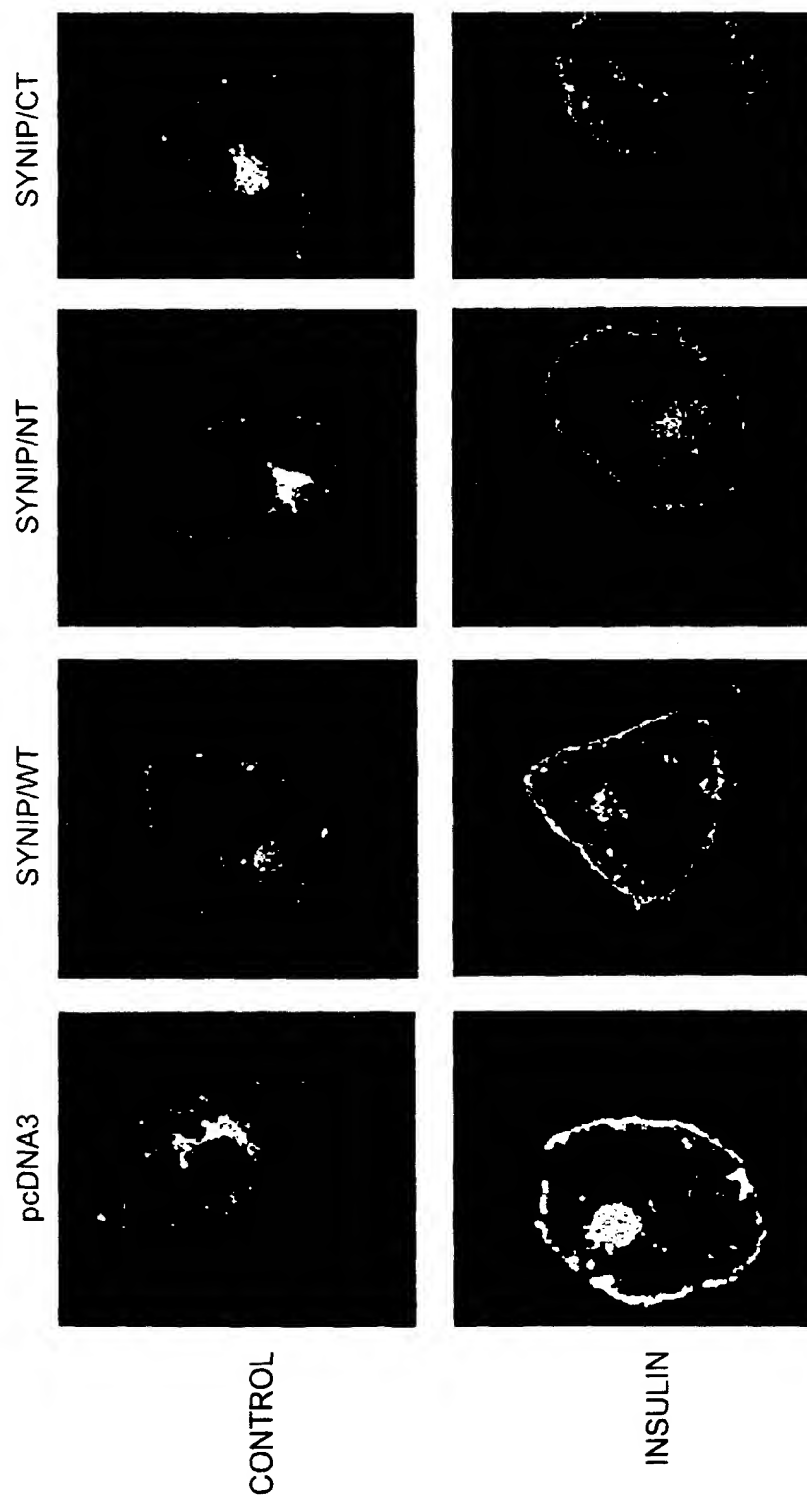
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FIG-5B GLUCOSE TRANSPORT



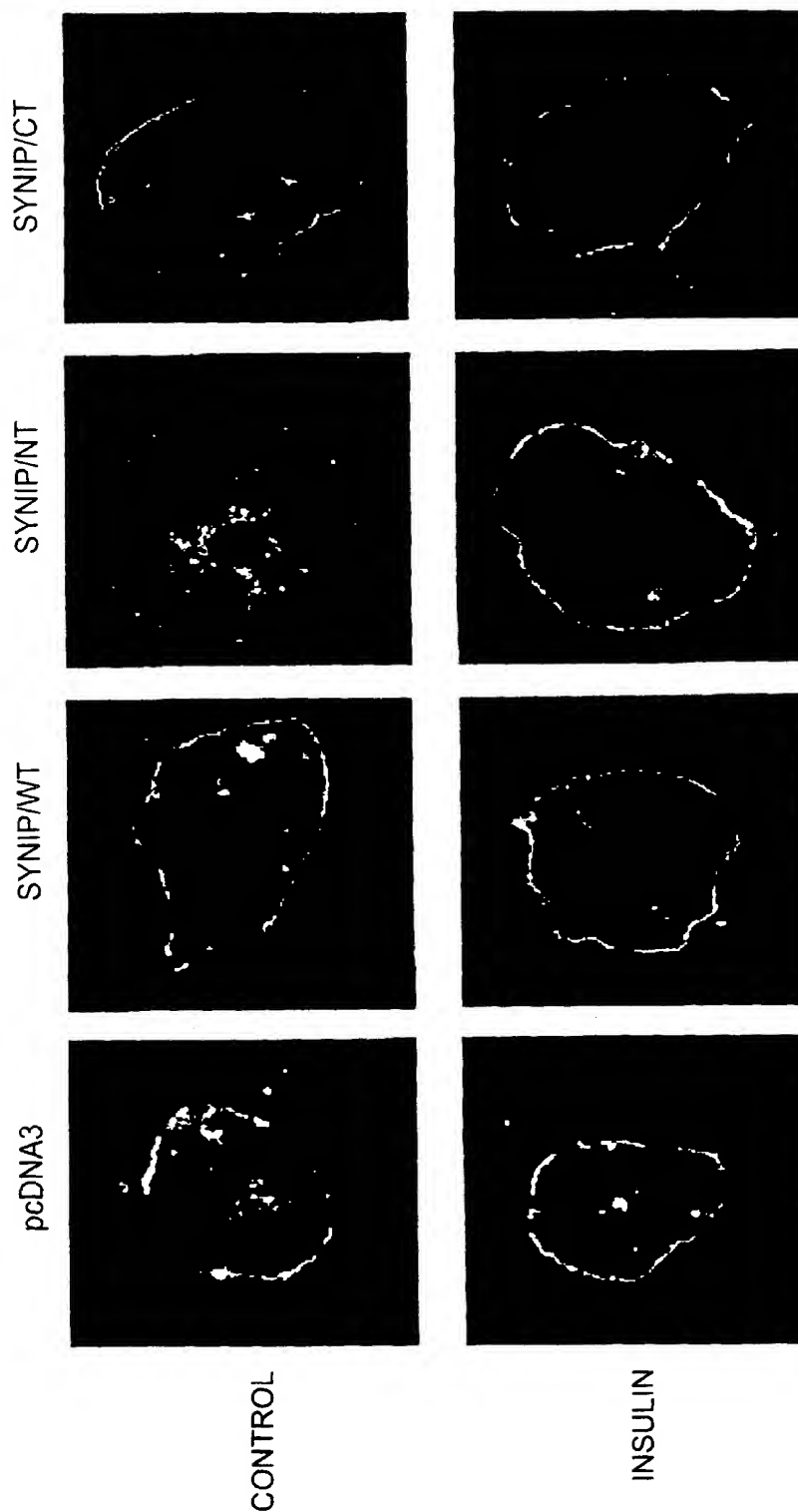
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FIG-6A GLUT4-eGFP



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FIG-6B_{eGFP-GLUT1}



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FIG-7

